

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent of : George Heavner, *et al.* Patent No.: 7,250,165
Serial No. : 09/920,137 Art Unit: 1647
Filed : August 1, 2001 Examiner: Seharaseyon, Jegatheesan
Title : Anti-TNF Antibodies, Compositions, Methods And Uses

Attention: Certificate of Corrections Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

REQUEST FOR CERTIFICATE OF CORRECTION UNDER 37 C.F.R. §1.322

Dear Sir:

Transmitted herewith is a Certificate of Correction for U.S. Patent 7,250,265, issued July 31, 2007. Upon review of the patent, the patentees noticed that the sequence listing published with the above-referenced patent does not correspond to the sequence listing provided to the U.S. Patent and Trademark Office, as set forth in the image file wrapper provided on PAIR (see January 17, 2006 sequence listing). The patentees submit that this error occurred due to actions of the U.S. Patent and Trademark Office, since the correct sequence listing was provided to the Office and considered by the examiner during prosecution. Accordingly, patentees request that the sequence listing be corrected as follows:

Column 73, line 21, delete the entire sequence listing through column 84, line 19 and
insert

--SEQUENCE LISTING

<210> 1

<211> 5

<212> PRT

<213> Homo sapiens

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<221> MISC_FEATURE

<222> (1)..(5)

<223> Heavy Chain complementarity determinng region 1 (CDR1).

<400> 1

Ser Tyr Ala Met His

1 5

<210> 2

<211> 17

<212> PRT

<213> Homo sapiens

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<221> MISC_FEATURE

<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 2 (CDR2).

<220>

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<222> (1)..(1)

<223> Xaa at position 1 is selected from Ile, Phe or Val.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is selected from Ile or Met.

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is selected from Ser or Leu.

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Tyr or Phe.

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is selected from Lys or Tyr.

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa at position 11 is selected from Ser or Tyr.

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

Xaa	Xaa	Xaa	Xaa	Asp	Gly	Ser	Asn	Lys	Xaa	Xaa	Ala	Asp	Ser	Val	Lys	Xaa
1		5			10			15								

<210> 3

<211> 17

<212> PRT

<213> Homo sapiens

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<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 3 (CDR3).

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Ile or Val.

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

Asp	Arg	Gly	Xaa	Xaa	Ala	Gly	Gly	Xaa	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
1			5			10			15							

<210> 4

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(11)

<223> Light Chain complementarity determinng region 1 (CDR1).

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa at position 7 is selected from Ser or Tyr.

<400> 4

Arg	Ala	Ser	Gln	Ser	Val	Xaa	Ser	Tyr	Leu	Ala
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<210> 5

<211> 7

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(7)

<223> Light Chain complementarity determinng region 2 (CDR2).

<400> 5

Asp Ala Ser Asn Arg Ala Thr

1 5

<210> 6

<211> 10

<212> PRT

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<222> (1)..(10)

<223> Light Chain complementarity determinng region 3 (CDR3).

<400> 6

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr

1 5 10

<210> 7

<211> 126

<212> PRT

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<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr

20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val

35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly

100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120 125

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<211> 108

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<213> Homo sapiens

<400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro

65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

<210> 9

<211> 157

<212> PRT

<213> Homo sapiens

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<222> (1)..(157)

<223> human TNF alpha monomer sequence

<400> 9

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
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Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
20 25 30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 10

<211> 18

<212> DNA

<213> Homo sapiens

<400> 10

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18

<210> 11

<211> 18

<212> DNA

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<400> 11

cacctgcact cggtgctt

18

<210> 12

<211> 30

<212> DNA

<213> Homo sapiens

<400> 12

cactgttttg agtgtgtacg ggcttaagtt

30

<210> 13

<211> 18

<212> DNA

<213> Homo sapiens

<400> 13

gccgcacgtg tggaagg

18

<210> 14

<211> 25

<212> DNA

<213> Homo sapiens

<400> 14

agtcaaggtc ggactggctt aagtt

25

<210> 15

<211> 28

<212> DNA

<213> Homo sapiens

<400> 15

gtgtgccct ctcacaatct tcgaattt

28

<210> 16

<211> 18

<212> DNA

<213> Homo sapiens

<400> 16

ggcggtagac tactcgtc

18

<210> 17

<211> 7

<212> PRT

<213> Homo sapiens

<400> 17

Met Asp Trp Thr Trp Ser Ile

1 5

<210> 18

<211> 35

<212> DNA

<213> Homo sapiens

<400> 18

tttcgtacgc caccatggac tggacctgga gcatc 35

<210> 19

<211> 34

<212> DNA

<213> Homo sapiens

<400> 19

tttcgtacgc caccatgggg ttgggctga gctg 34

<210> 20

<211> 35

<212> DNA

<213> Homo sapiens

<400> 20

tttcgtacgc caccatggag ttgggctga gcatg 35

<210> 21

<211> 35

<212> DNA

<213> Homo sapiens

<400> 21

tttcgtacgc caccatgaaa cacctgtggt tcttc 35

<210> 22

<211> 35

<212> DNA

<213> Homo sapiens

<400> 22

tttcgtacgc caccatgggg tcaaccgcca tcttc 35

<210> 23

<211> 6

<212> PRT

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<400> 23

Thr Val Thr Val Ser Ser

1 5

<210> 24

<211> 36

<212> DNA

<213> Homo sapiens

<400> 24

gtgccagtgg cagaggagtc cattcaagct taagtt

36

<210> 25

<211> 5

<212> PRT

<213> Homo sapiens

<400> 25

Met Asp Met Arg Val

1 5

<210> 26

<211> 31

<212> DNA

<213> Homo sapiens

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tttgtcgaca ccatggacat gagggctctc c

31

<210> 27

<211> 28

<212> DNA

<213> Homo sapiens

<400> 27

ttgtcgaca ccatggaagc cccagctc

28

<210> 28

<211> 6

<212> PRT

<213> Homo sapiens

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Thr Lys Val Asp Ile Lys

1 5

<210> 29

<211> 41

<212> DNA

<213> Homo sapiens

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ctggtttcac ctatagtttg cattcagaat tcggcgctt t

41

<210> 30

<211> 35

<212> DNA

<213> Homo sapiens

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catctccaga gacaattcca agaacacgct gtatc

35

<210> 31

<211> 35

<212> DNA

<213> Homo sapiens

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gtagaggctc ctgttaaggt tctgtgcga catag

35

<210> 32

<211> 19

<212> PRT

<213> Homo sapiens

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<222> (1)..(19)

<223> Signal sequence for heavy chain variable region sequences as presented in
original Figure 4

<400> 32

Met Gly Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly

1 5 10 15

Val Gln Cys

<210> 33

<211> 20

<212> PRT

<213> Homo sapiens

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<221> MISC_FEATURE

<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in original Figure 5

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro

1 5 10 15

Asp Thr Thr Gly

20

<210> 34

<211> 428

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

<400> 34

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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120
tgtgcagcct ctggttcacc ttcaatagct atgctatgca ctgggtccgc caggctccgg 180
caaggggctg gagggtggg cagttatc atagatgga aaataaatac tacgcagact 240
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgta tctgcaaagt 300
aacagccaga gctgaggaca cggctgtgta ttactgtgcg agagatcgag gtatatcagc 360
aggtggaata ctactactac tacggtatgg acgtctgggg gcaagggacc acggtcaccg 420
tctctca
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428

<210> 35

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(387)

<223> light chain variable region DNA sequences as presented in original Figure 3

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ctctcctgca gggccagtcg gagggttagc agctacttag cctggtacca acagaaacct 180
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catccagcc 240
agggtcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 300
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccatt cacttcggc 360
cctgggacca aagtggatat caaacgt
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387

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Since the errors needing correction were due to U.S. Patent and Trademark Office mistakes, no fee is due under 35 U.S.C. §254. Should any fees be due for entry and consideration of this Certificate of Correction that have not been accounted for, the

Application No.: 09/920,137
Patent No.: 7,250,165

Docket No.: CEN 0250USNP

Commissioner is hereby authorized to charge Johnson & Johnson Deposit Account No. 10-0750/CEN0250NP/KJD. If there are any additional charges or credits in connection with this filing, the Commissioner is hereby authorized to charge/credit the Johnson & Johnson deposit account listed above.

Respectfully submitted,

____/Kenneth J. Dow/_____
Kenneth J. Dow
Attorney for Patentees
Reg. No. 32,890

Johnson & Johnson
One Johnson & Johnson Plaza
New Brunswick, NJ 08933-7003
(610) 651-7422
Dated: March 25, 2009